Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

- 1. (Currently amended) A method for the detection of cytosine methylations methylation in DNA is hereby characterized in that comprising the steps of:
- a) <u>bringing</u> the DNA to be investigated is brought into contact with a cytidine deaminase, whereby the cytidine deaminase deaminates cytidine and 5-methylcytidine at different rates,
- b) investigating the partially deaminated DNA is investigated with respect to its sequence, and
- c) <u>concluding</u>, from the presence or the proportion of deaminated positions, conclusions can be made on the methylation status of the DNA to be investigated in said positions.
- 2. (Currently amended) The method according to claim 1, further characterized in that activation-induced cytidine deaminase—AID or a biologically active fragment of AID or a modification thereof can be used as the methylation-specific wherein the enzyme AID (activation-induced cytidine deaminase) is used as the cytidine deaminase.
- 3. (Currently amended) The method according to claim 1, further characterized in that wherein the DNA to be investigated is present at least partially in single-stranded form.
- 4. (Currently amended) The method according to claim 1, further characterized in that

<u>comprising hybridizing</u> the DNA to be investigated <u>hybridizes</u> with oligomers, whereby the hybrids are present in single-stranded form at the cytosine positions under investigation.

- 5. (Currently amended) The method according to claim 4, further characterized in that wherein the single-stranded regions are between 3 and 20 nucleotides long.
- 6. (Currently amended) The method according to claim 4, further characterized in that wherein the single-stranded regions are between 5 and 12 nucleotides long.
- 7. (Currently amended) The method according to claim 4, further characterized in that wherein the single-stranded region is 9 nucleotides long.
- 8. (Currently amended) The method according to claim 1 4, further characterized in that the wherein the oligomers have a length of 20 to 150 nucleotides.
- 9. (Currently amended) The method according to claim 4 <u>4</u>, further characterized in that the wherein the oligomers have a length of 35 to 60 nucleotides.
- 10. (Currently amended) The method according to claim 4, further characterized in that wherein the oligomers are present in a concentration of 1 pM to 1000 nM.

- 11. (Currently amended) The method according to claim 4, further characterized in that wherein the oligomers are present in a concentration of 1 nM to 100 nM.
- 12. (Currently amended) The method according to claim 1, further characterized in that comprising amplifying the DNA to be investigated is amplified after the enzyme treatment.
- 13. (Currently amended) The method according to claim 12, further characterized in that wherein the amplification is conducted by means of amplifying step comprises conducting a polymerase reaction.
- 14. (Currently amended) The method according to claim 13, further characterized in that wherein the amplification is conducted by means of amplifying step comprises conducting a polymerase chain reaction.
- 15. (Currently amended) The method according to claim 14, further characterized in that wherein the polymerase chain reaction is conducted by means of comprises using methylation-specific primers.
- 16. (Currently amended) The method according to claim 14, further characterized in that wherein the polymerase chain reaction comprises utilizing at least one methylation-specific blocker oligomer is utilized in the polymerase chain reaction.

- 17. (Withdrawn) The method according to claim 12, further characterized in that a repeated enzymatic conversion with a cytidine deaminase is conducted after the amplification.
- 18. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by means of methods of length measurement, mass spectrometry or sequencing.
- 19. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by means of the primer extension method.
- 20. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by hybridization to oligomer arrays.
- 21. (Currently amended) The method according to claim 12, further characterized in that comprising analyzing the amplificates are analyzed with the use of real-time variants.
- 22. (Currently amended) The method according to claim 21, further characterized in that wherein the analyzing step comprises conducting a Tagman or a Lightcycler method is conducted.
- 23. (Withdrawn) The method according to claim 12, further characterized in that several fragments are simultaneously amplified by means of a multiplex reaction.

- 24. (Withdrawn) Use of a method according to claim 1 for the diagnosis of cancer diseases or other disorders associated with a change in the methylation status.
- 25. (Withdrawn) Use of a method according to claim 1 for predicting undesired drug interactions, for the differentiation of cell types and tissues or for the investigation of cell differentiation.
- 26. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for methylation analysis.
- 27. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for the diagnosis of cancer diseases or other disorders associated with a change in the methylation status.
- 28. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for predicting undesired drug interactions, for the differentiation of cell types and tissues or for the investigation of cell differentiation.
- 29. (Withdrawn) Use according to claim 24, further characterized in that the cytidine deaminase involves activation-induced cytidine deaminase (AID), a biologically active fragment of AID or a modification thereof.

30. (Withdrawn) A kit, which comprises the AID enzyme, a biologically active fragment of AID or a modification thereof as well as oligomers and the buffers necessary for the deamination, as well as optionally also a polymerase, primers and probes for an amplification and detection.